

SEQUENCE LISTING

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GENERAL INFORMATION

<110> APPLICANT: Lingappa, Jaisri
Lingappa, Vishwanath

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<120> TITLE OF THE INVENTION: HIV Capsid Assembly Associated
Compositions and Method

<130> FILE REFERENCE LING.001.01US

<140> CURRENT APPLICATION NUMBER:

<141> CURRENT FILING DATE: 2002-01-02

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COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: PatentIn version 3.1

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/020,144

FILING DATE: 06-FEB-1998

<160>NUMBER OF SEQUENCES: 6

<170> PatentIn Version 3.0

<210>INFORMATION FOR SEQ ID NO:1

SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1610 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(C) ISOLATE: DNA coding sequence for HIV capsid protein Pr55

<400> SEQUENCE DESCRIPTION: SEQ ID NO:1

ATGGGTGCGA	GAGCGTCGGT	ATTAAGCGGG	GGAGAATTAG	ATAAATGGGA	AAAAATTCGG	60
TTAAGGCCAG	GGGGAAGAA	AAAATATAAG	TTAAACATA	TAGTATGGGC	AAGCAGGGAG	120
CTAGAACGAT	TCGCAGTCAA	TCCTGGCCTG	TTAGAAACAT	CAGAAGGCTG	CAGACAAATA	180
TTGGGACAGC	TACAGCCATC	CCTTCAGACA	GGATCAGAAG	AACTTAGATC	ATTATATAAT	240
ACAGTAGCAA	CCCTCTATTG	TGTACATCAA	AGGATAGATG	TAAAAGACAC	CAAGGAAGCT	300
TTAGAGAAGA	TAGAGGAAGA	GCAAAACAAA	AGTAAGAAAA	AGGCACAGCA	AGCAGCAGCT	360
GCAGCTGGCA	CAGGAAACAG	CAGCCAGGTC	AGCCAAAATT	ACCCTATAGT	GCAGAACCTA	420
CAGGGGCAAA	TGGTACATCA	GGCCATATCA	CCTAGAACTT	TAAATGCATG	GGTAAAAGTA	480
GTAGAAGAAA	AGGCTTTCAG	CCCAGAAGTA	ATACCCATGT	TTTCAGCATT	ATCAGAAGGA	540
GCCACCCAC	AAGATTTAAA	CACCATGCTA	AACACAGTGG	GGGGACATCA	AGCAGCCATG	600
CAAATGTTAA	AAGAGACTAT	CAATGAGGAA	GCTGCAGAAT	GGGATAGAGT	GCATCCAGTG	660
CATGCAGGGC	CTATTGCACC	AGGCCAAATG	AGAGAACCAA	GGGGAAGTGA	CATAGCAGGA	720
ACTACTAGTA	CCCTTCAGGA	ACAAATAGGA	TGGATGACAA	ATAATCCACC	TATCCCAGTA	780
GGAGAAATCT	ATAAAAGATG	GATAATCCTG	GGATTAAATA	AAATAGTAAG	AATGTATAGC	840
CCTACCAGCA	TTCTGGACAT	AAGACAAGGA	CCAAAGGAAC	CCTTTAGAGA	TTATGTAGAC	900
CGGTTCTATA	AAACTCTAAG	AGCCGAACAA	GCTTCACAGG	ATGTAAAAAA	TTGGATGACA	960
GAAACCTTGT	TGGTCCAAAA	TGCAAACCCA	GATTGTAAGA	CTATTTTAAA	AGCATTGGGA	1020
CCAGCAGCTA	CACTAGAAGA	AATGATGACA	GCATGTCAGG	GAGTGGGGGG	ACCCGGCCAT	1080
AAAGCAAGAG	TTTTGGCTGA	AGCCATGAGC	CAAGTAACAA	ATCCAGCTAA	CATAATGATG	1140
CAGAGAGGCA	ATTTTAGGAA	CCAAAGAAAG	ACTGTTAAGT	GTTTCAATTG	TGGCAAAGAA	1200
GGGCACATAG	CCAAAAATTG	CAGGGCCCCT	AGGAAAAAGG	GCTGTTGGAG	ATGTGGAAGG	1260
GAAGGACACC	AAATGAAAGA	TTGCACTGAG	AGACAGGCTA	ATTTTTTAGG	GAAGATCTGG	1320
CCTTCCTACA	AGGGAAGGCC	AGGGAATTTT	CTTCAGAGCA	GACCAGAGCC	AACAGCCCCA	1380
CCAGAAGAGA	GCTTCAGGTT	TGGGGAGGAG	AAAACAACCTC	CCTCTCAGAA	GCAGGAGCCG	1440

ATAGACAAGG AACTGTATCC TTAACTTCC CTCAGATCAC TCTTTGGCAA CGACCCCTCG 1500
TCACAATAAG GATAGGGGGG CAACTAAAGG AAGCTCTATT AGATACAGGA GCAGATGATA 1560
CAGTATTAGA AGAAATGAAT TTGCCAGGAA AATGGAAACC AAAAATGATA 1610

5 <210> INFORMATION FOR SEQ ID NO:2

SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: PRT

(vi) ORIGINAL SOURCE:

(C) ISOLATE: peptide fragment of host cell (wheat germ) protein

15 HP68

<400> SEQUENCE DESCRIPTION: SEQ ID NO:2

Pro Arg Pro Tyr Leu Asp Val Lys Gln Arg Leu Lys Ala Ala Arg Val

1 5 10 15

Ile Arg Ser Leu Leu Arg Ser Asn

20

25 <210> INFORMATION FOR SEQ ID NO:3

SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(C) ISOLATE: Degenerate oligonucleotide C-terminal peptide

35 sequence of WGHP68

<400> SEQUENCE DESCRIPTION: SEQ ID NO:3

ATGAATTCAC TGGGACTGCG GATAGATTAC TGGTACTGGG GATC 44

40

<210> INFORMATION FOR SEQ ID NO:4

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(C) ISOLATE: Degenerate oligonucleotide C-terminal peptide
sequence of WGHP68

<400> SEQUENCE DESCRIPTION: SEQ ID NO:4

ATGAATTCAC TGGGCTCTGA TAGATTACTG GTACTGGGGA TC 42

<210> SEQ ID NO:5

<211> Length:604

<212> Type: PRT

<213> Organism: Triricum aestivum

<400> Sequence 5

Met Ala Asp Arg Leu Thr Arg Ile Ala Ile Val Ser Glu Asp Lys Cys
1 5 10 15
Lys Pro Lys Lys Cys Arg Gln Glu Cys Lys Lys Ser Cys Pro Val Val
20 25 30
Lys Thr Gly Lys Leu Cys Ile Glu Val Ser Pro Val Ala Lys Leu Ala
35 40 45
Phe Ile Ser Glu Glu Leu Cys Ile Gly Cys Gly Ile Cys Val Lys Lys
50 55 60
Cys Pro Phe Asp Ala Ile Glu Ile Ile Asn Leu Pro Lys Asp Leu Glu
65 70 75 80
Lys Asp Thr Thr His Arg Tyr Gly Pro Asn Thr Phe Lys Leu His Arg
85 90 95
Leu Pro Val Pro Arg Pro Gly Gln Val Leu Gly Leu Val Gly Thr Asn
100 105 110
Gly Ile Gly Lys Ser Thr Ala Leu Lys Val Leu Ala Gly Lys Leu Lys
115 120 125
Pro Asn Leu Gly Arg Phe Lys Asn Pro Pro Asp Trp Gln Glu Ile Leu
130 135 140

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Thr Tyr Phe Arg Gly Ser Glu Leu Gln Asn Tyr Phe Thr Arg Ile Leu
 145 150 155 160
 Glu Asp Asn Leu Lys Ala Ile Ile Lys Pro Gln Tyr Val Asp His Ile
 165 170 175
 5 Pro Lys Ala Val Gln Gly Asn Val Gly Gln Val Leu Glu Gln Lys Asp
 180 185 190
 Glu Arg Asp Met Lys Asn Glu Leu Cys Val Asp Leu Glu Leu Asn Gln
 195 200 205
 Val Ile Asp Arg Asn Val Gly Asp Leu Ser Gly Gly Glu Leu Gln Arg
 10 210 215 220
 Phe Ala Ile Ala Val Val Ala Val Gln Ser Ala Glu Ile Tyr Met Phe
 225 230 235 240
 Asp Glu Pro Ser Ser Tyr Leu Asp Val Lys Gln Arg Leu Lys Ala Ala
 245 250 255
 15 Arg Val Ile Arg Ser Leu Leu Arg Ser Asn Ser Tyr Val Ile Val Val
 260 265 270
 Glu His Asp Leu Ser Val Leu Asp Tyr Leu Ser Asp Phe Ile Cys Cys
 275 280 285
 Leu Tyr Gly Lys Pro Gly Ala Tyr Gly Val Val Thr Leu Pro Phe Ser
 20 290 295 300
 Val Arg Glu Gly Ile Asn Ile Phe Leu Ala Gly Phe Val Pro Thr Glu
 305 310 315 320
 Asn Leu Arg Phe Arg Asp Glu Ser Leu Thr Phe Lys Ile Ala Glu Thr
 325 330 335
 25 Gln Glu Ser Ala Glu Glu Val Ala Thr Tyr Gln Arg Tyr Lys Tyr Pro
 340 345 350
 Thr Met Ser Lys Thr Gln Gly Asn Phe Lys Leu Ser Val Val Glu Gly
 355 360 365
 Glu Phe Thr Asp Ser Gln Ile Val Val Met Leu Gly Glu Asn Gly Thr
 30 370 375 380
 Gly Lys Thr Thr Phe Ile Arg Met Leu Ala Gly Leu Leu Lys Pro Asp
 385 390 395 400
 Thr Met Glu Gly Thr Glu Val Glu Ile Pro Glu Phe Asn Val Ser Tyr
 405 410 415
 35 Lys Pro Gln Lys Ile Ser Pro Lys Phe Gln His Pro Val Arg His Leu
 420 425 430
 Leu His Ser Lys Ile Arg Asp Ser Tyr Thr His Pro Gln Phe Val Ser
 435 440 445
 Asp Val Met Lys Pro Leu Gln Ile Glu Gln Leu Met Asp Gln Glu Val
 40 450 455 460
 Ile Asn Leu Ser Gly Gly Glu Leu Gln Arg Val Ala Leu Cys Leu Cys

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465 470 475 480
Leu Gly Lys Pro Ala Asp Ile Tyr Leu Ile Asp Glu Pro Ser Ala Tyr
 485 490 495
Leu Asp Ser Glu Gln Arg Ile Val Ala Ser Lys Val Ile Lys Arg Phe
5 500 505 510
Ile Leu His Ala Lys Lys Thr Ala Phe Ile Val Glu His Asp Phe Ile
 515 520 525
Met Ala Thr Tyr Leu Ala Asp Lys Val Ile Val Tyr Glu Gly Leu Ala
 530 535 540
10 Ser Ile Asp Cys Thr Ala Asn Ala Pro Gln Ser Leu Val Ser Gly Met
545 550 555 560
Asn Lys Phe Leu Ser His Leu Asp Ile Thr Phe Arg Arg Asp Pro Thr
 565 570 575
Asn Tyr Arg Pro Arg Ile Asn Lys Leu Glu Ser Thr Lys Asp Arg Glu
 580 585 590
15 Gln Lys Asn Ala Gly Ser Tyr Tyr Tyr Leu Asp Asp
 595 600

<210> SEQ ID NO:6

<211> LENGTH: 599

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE 6

25 Met Ala Asp Lys Leu Thr Arg Ile Ala Ile Val Asn His Asp Lys Cys
1 5 10 15
Lys Pro Lys Lys Cys Arg Gln Glu Cys Lys Lys Ser Cys Pro Val Val
 20 25 30
Arg Met Gly Lys Leu Cys Ile Glu Val Thr Pro Gln Ser Lys Ile Ala
30 35 40 45
Trp Ile Ser Glu Thr Leu Cys Ile Gly Cys Gly Ile Cys Ile Lys Lys
50 55 60
Cys Pro Phe Gly Ala Leu Ser Ile Val Asn Leu Pro Ser Asn Leu Glu
65 70 75 80
35 Lys Glu Thr Thr His Arg Tyr Cys Ala Asn Ala Phe Lys Leu His Arg
 85 90 95
Leu Pro Ile Pro Arg Pro Gly Glu Val Leu Gly Leu Val Gly Thr Asn
 100 105 110
Gly Ile Gly Lys Ser Ala Ala Leu Lys Ile Leu Ala Gly Lys Gln Lys
40 115 120 125
Pro Asn Leu Gly Lys Tyr Asp Asp Pro Pro Asp Trp Gln Glu Ile Leu

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	130	135	140	
	Thr Tyr Phe Arg Gly Ser Glu Leu Gln Asn Tyr Phe Thr Lys Ile Leu			
	145	150	155	160
	Glu Asp Asp Leu Lys Ala Ile Ile Lys Pro Gln Tyr Val Ala Arg Phe			
5	165	170	175	
	Leu Arg Leu Ala Lys Gly Thr Val Gly Ser Ile Leu Asp Arg Lys Asp			
	180	185	190	
	Glu Thr Lys Thr Gln Ala Ile Val Cys Gln Gln Leu Asp Leu Thr His			
	195	200	205	
10	Leu Lys Glu Arg Asn Val Glu Asp Leu Ser Gly Gly Glu Leu Gln Arg			
	210	215	220	
	Phe Ala Cys Ala Val Val Cys Ile Gln Lys Ala Asp Ile Phe Met Phe			
	225	230	235	240
	Asp Glu Pro Ser Ser Tyr Leu Asp Val Lys Gln Arg Leu Lys Ala Ala			
15	245	250	255	
	Ile Thr Ile Arg Ser Leu Ile Asn Pro Asp Arg Tyr Ile Ile Val Val			
	260	265	270	
	Glu His Asp Leu Ser Val Leu Asp Tyr Leu Ser Asp Phe Ile Cys Cys			
	275	280	285	
20	Leu Tyr Gly Val Pro Ser Ala Tyr Gly Val Val Thr Met Pro Phe Ser			
	290	295	300	
	Val Arg Glu Gly Ile Asn Ile Phe Leu Asp Gly Tyr Val Pro Thr Glu			
	305	310	315	320
	Asn Leu Arg Phe Arg Asp Ala Ser Leu Val Phe Lys Val Ala Glu Thr			
25	325	330	335	
	Ala Asn Glu Glu Glu Val Lys Lys Met Cys Met Tyr Lys Tyr Pro Gly			
	340	345	350	
	Met Lys Lys Lys Met Gly Glu Phe Glu Leu Ala Ile Val Ala Gly Glu			
	355	360	365	
30	Phe Thr Asp Ser Glu Ile Met Val Met Leu Gly Glu Asn Gly Thr Gly			
	370	375	380	
	Lys Thr Thr Phe Ile Arg Met Leu Ala Gly Arg Leu Lys Pro Asp Glu			
	385	390	395	400
	Gly Gly Glu Val Pro Val Leu Asn Val Ser Tyr Lys Pro Gln Lys Ile			
35	405	410	415	
	Ser Pro Lys Ser Thr Gly Ser Val Arg Gln Leu Leu His Glu Lys Ile			
	420	425	430	
	Arg Asp Ala Tyr Thr His Pro Gln Phe Val Thr Asp Val Met Lys Pro			
	435	440	445	
40	Leu Gln Ile Glu Asn Ile Ile Asp Gln Glu Val Gln Thr Leu Ser Gly			
	450	455	460	

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Gly Glu Leu Gln Arg Val Arg Leu Arg Leu Cys Leu Gly Lys Pro Ala
465 470 475 480

Asp Val Tyr Leu Ile Asp Glu Pro Ser Ala Tyr Leu Asp Ser Glu Gln
485 490 495

5 Arg Leu Met Ala Ala Arg Val Val Lys Arg Phe Ile Leu His Ala Lys
500 505 510

Lys Thr Ala Phe Val Val Glu His Asp Phe Ile Met Ala Thr Tyr Leu
515 520 525

Ala Asp Arg Val Ile Val Phe Asp Gly Val Pro Ser Lys Asn Thr Val
10 530 535 540

Ala Asn Ser Pro Gln Thr Leu Leu Ala Gly Met Asn Lys Phe Leu Ser
545 550 555 560

Gln Leu Glu Ile Thr Phe Arg Arg Asp Pro Asn Asn Tyr Arg Pro Arg
565 570 575

15 Ile Asn Lys Leu Asn Ser Ile Lys Asp Val Glu Gln Lys Lys Ser Gly
580 585 590

Asn Tyr Phe Phe Leu Asp Asp
595

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WHAT IS CLAIMED IS: